

; Sequence 12, Application US/10030203
; GENERAL INFORMATION:
; APPLICANT: Alán Garen
; APPLICANT: Zhiwei Hu
; TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
; FILE REFERENCE: OCR-679B.US
; CURRENT APPLICATION NUMBER: US/10/030,203
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/US00/16481
; PRIOR-FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: MS DOS
; SEQ ID NO 12
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: hfvliasm immunoconjugate
; OTHER INFORMATION: includes leader + hfvliasm + human IgG1FC
US-10-030-203-12.11
KLCRDFIMVSOALRLGLLGLGQCLAGVAKASGETRDMPPKPGHVRVFTOEAHGVLLHRRRANA
FLEELRPGSLERECEKBOCSFEAREIKPKAERTKLFWISYSDGQOCASSPCONGSKCKOLOSVCFL
PAFEGRCETHKDDOLI CWNENGCEYOCSDTHTKSCRCRCHGYSLLADGVSCTVPEYPCGKPILEK
RNASKPQRI VGGKVCYPCGECBQVLLVNGAQLCGGLTINTI WVWSAAHCFDKIKNWRNLI AIVGEHDL
SEHDDEQSRVAQVIFISTVYVPGTTHDIALRLHPQVLTLDHVPLCLPERTSERTLAFVRFSLVSG
WGQLLDRGATALELVANVPLMTQDCLQOSKRGDSPNITREYMCAGYSDGSKDCAGDSGGPHATHYR
GTWYLTGTVWGOGCATVGHFGVTVRSQYIEWLOKLMREBPRPGVLLRAAPPFGSAEPKSCDKTHCTPC
PAPELLGSPVLPFPKPKOTLMSITREVTCTVVDVSHEDDEVKFNVTVDGVEVHXAKTKREEQYNST
YRVSVLTVLHQDLNGKEYCKCKSNKALPAPIEKTI SKAKGPXREXQVYITLPPSRDELTKNQVSLTCLV
KGFPSDIAVVENESNGQPPENNYKTTTPPVLDSGSPFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTK
SLSLSPGKXXAA1

US-10-030-203-12.2
SFAEISSNSPRSGSSAFCFLPRAAWLQAGSLRPOEEKHCTCRSGRLTESXPRKPTASTCTGAGATPR
SWRSCGRAPWRGARRSAPSRRGRSRRTRRSGCSGLTVMGTSVPOVHARMGAPARTSSPSISASAS
LPSSRAQTVTRMTSXTXVKTAAVSTASTVAPVTRAPSAFVGTLCWQTCGPAHPQLNIHVKEYLFXKK
EMPANPKAELMGARCAPKSGSCVWMLSCVCGXSTPSGWSPRETVTSKRTGTGXSRCWASTTS
ASTGMSRAGWRSSSIPARTPTTTRSCACTSPWSLSLTMCPSCAPNGRSLRGRWPS CASHWSAA
GASCTVAPRPMSSCTCGXXPTACSHGRWETPOISRSTCSVPATMAARTPARCTVEAHMPPPTTG
ARGTXRASSAGAAQPNATLCTGSPSTSGGSKSSCAQSHAQSSCEPHFPDQSPNLVTKLTHAHRA
QHLNSWGRQSSQNPRTPSXSGPLURSHAWMTXATKLRSSTSTGTWTAWRCIXPQSRGRSSTHAR
TWSASSPSCRTGMARSTARSPTKSPSPSRKPSKPGKSPENXRCCTCPHPGMSXPRTRSAXPWS
KASIPATSPWSGRAMGSRRTTTRPRLPCWPTPTAPSSSTASSPWTBAGSRGTS SHAPXCMRLCTTTTTRR
ASPCULRVNDKRP1

US-10-030-203-12.3
ALQRFHGLPGQAPLPSAWASGLPGCRRGRXGLRRNTGHAVEAGASOSLNRNPGSPRRPAPAPARQV
PGAAAGLPGEGVQGVALLRGCGDLOGGDEDAVLDFLOXWGPVCLKSMPEWLLOGPAPVLYLLLP
CLRGPELDAQOXPADLCERERRLXAVLQXPHGHQALLSVPRGVLISAGRVLHTHSXI SMWNKTSYRKK
KCOQTPRNCGGQVPGRGVWAGVVGWSDPDQHLGLRGLPLFRQNOLEBPDGRGAGRARPO
RARRCXARPAGAGHHPQHVPGHQRHRAAPPAPARGPHXPCGAPLPARTDVLKEDAGLRALLIGORL
GPAAGPWRHGPAGAHGAQAPADDPGLPAAVTEGGRLPKYHGVHVCRLLCWOQGLLRGCQWRPTCHPLPG
HVVPDGRQOLGRLNGLMVGHQLPVHRAAKAHARATRPSPAPSPISIRIRAQILXONSHMPTVP
STXTPGGTVSLPLPKTQGHDPDLPXGHMGREPRRPGXQVLVGRREGGAXCDQKAAAGPQVQHV
PCQGRPHRAPALAEWQVQVQLOQSPSPHRENHLOSRAAPRTTGVHPAPIPGXADQEPGQDLPQ
RLLSQRHRRGVGEQWAAEQLODHASRACLRLLLPLQAHRGQEQVAAGERLLMLRDXGSAQPLHABE
PLPVSGXMSGI

US-10-030-203-12.4
AAAYHLPGDRERLFCVXMLCRASCITEHEKTPCCCHLLSTVLSLXKRKEPSESSTGGVVLXLFSGCPLL
SWRTAMSLCXKPLTVQLVRLTWLVSRRDGRGVYTCXSGCPLALEMVFMSGAGRALLLTLHLSLFPQSG
SWCRTVRLTTRYVLLYCSRRGFVLAXCTTSTYQNLNTSGSSMLTSTTHVTSGREIMRVSLGFGGK
RKTDPGPRSSGAGHGVXVLSQDLSGADPGNGARRTPGRGSRWSFCGSHMYETLVYTPKMTVAQP
WPQLTWVRYHVPRXWACGPSPAPQSLSEXPQNMYSVIFGESPTFRDCCQSWISRGTLSTWS
SHAVAPRSSSPQPLTNEKRTKLSVLSNVRSGRGTITWVRITTCWCRSWSMLVVPVTYVILGMMTC
ATRLRCLSPSCSLRSCSPSTAIRFLQFLLSQWAAETTMVLIIRVPHNXAPPTNNRTCHGHSPLGHTL
PTTIRPWGLLAFLSRIGIFPHGYSTVQODTSPASREYPSWHROERLVPVMSLOYSQOPSPSTQISWS
SILCVSQFRPSKAGROKQIXDWMSVLEQPPFWHGLAHWSPLXIQNSFVLSASLKI SRASSKEHCSSLH
SLSRFPGRSSSNLARRRRCRTPWASSWVTYTLGPGPHGMSVSPPEALATPPAARQPSXPSRRQRS
RAWETMMSLSQSI

US-10-030-203-12.5

RPLIITYPETGRSSACSCABPHASRRMRRSPATCSPRXACCRRRRRSPAREAWSCSCSPPAHC
PTPRRCWRDRSLXPGRSXGPGSWAHGPGWAGCTPVILGAALMLWRFSRMLGGLCWRPCTCTCHSAS
PGAGRGXPHGTCCCTAPPAALSWYAPRRRPTSTXPOGLRGRSPPRMXPOGSGRSXGCPVILGR
GRLTVPCGVQVLTGVMCFCHKI WALRI REMGLAGLLGVALSAXAFAA TCTGRPWC TPOSGPRLRSP
GPSXRCPSGTTTCGSGWHVGLHCPRRSPCCCHPSRHRHTCTPYLGLSLPPSVTAAGSPGSSAGAXAPXA
PGPMRHGPAAGFSPRXPMSARRPASSQRTSVRAGSAPHGQXPRAGAGAAARGMWC PGRTCMGXFXPA
PPAGSAHPRRARXGRAPAPRSGSSSFCRNSGPRPRWCXSGSPHTTELHSTPTGAMDTPLWGTFC
PPQFLGVYCHWFFLEXYFHMDIQLMWYCRTPLPAESTPRGTDRSAWPCGCHCTAHSRRSRHSAGH
PCASHSSGPRQGRSRYRTGAGPCRSPHSGMDLRHTGPHCKRGTASSTASSPRXRSPPGPRRSTAPCT
PSGSPAAAPCTRWRRAGAGARRGLPGLRLRCEAPASTACTPVFLLLRXPRLPQSGSPEAQAEGRGAX
GPGRFXXNLCA1

US-10-030-203-12.6
GRLSFTRRQGEALLRVVVVQSLMHHGAXEDVPLLPALVHGELAVEBEGAVGVGHRRGLVVVLRPLIAL
PLHGDVAGIEAFDQAGQADLVLGQLIPGWCQCCHLXFSGLPFGDGLDGWEGFVGDLALVLAIQV
LVQDGEDADHTVRAVVLPLRLCLGXMHHAHVHVELDLRVFAVHHHACDLRGPDGHEGVHAGCAAL
EDXSPOEFRCWARWACVSVFTRFGLCGSGKWSQEDSWMLXAHELLQPLDVLGDGPGVHPKVAHGCAAL
APADDARQVPRAPVVGGMWASTVPRAGVLAALIRVAGTEHVLDRDIMGVSHLPLXLLQAVLHQHGHVEHEL
QGRGATVQOLPAADQDXEAHEGQRLRBRPFGQAEHGMHVEDHGLVQAEOQRDVVVGARDVRAGDDDR
HPPALLIIPVLAEVVLAQHRDQVPPVLDVFVETVGRGDHPDGVDDQGPPTQLSSIHQOQDLPTWLPFGAHLI
PHNSALGPAGISFFXNRVFTWIFNCGCAGHPVCCQRPVLAFTGALGARVVTA VLLTAALVHLDQLVI
LVRLTVPALEGREAEADIGLELVLGAPILAWTXGLVPI TVRNPEQLRPLRVLEDLPGLLEGALLLAL
PLQGARPOLLOERVGAPAPVQDAVGLFLGYEDSVTRPLRPHVPCFSSXGLSDPACSQALPKPKAEEBE
GLGDHDEISAK1

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LHNHYTKSLSPGK
 AXEDVLLPPALVHGLAVEBEGAVGVQHRGRLVVLRPIALPLHGDVAGIEAFDAQADLVLGOLIPG
 30 40 X 50 60 70 80 90
 WQGVHLXPSGLPFGDGLDGGWEGFVGDALVLLAIQVVLVQDGEDADHTYRAVLLPLRLCLGXMHILH
 100 110 120 130 140 150 160 170
 AVHPVELDLRVFAVHHHACDLRPGDHEGVLFWGEEDXRSPQBFRCWARWACVSYFTRFGLCGSGKW
 180 190 200 210 220 230 240
 GSQEDSWALXAHELLQPLDVLGDPGVHPKVAHGAALAPADDAPOVPRAPVVGGMWASTVPRAGVLAIRV
 250 260 270 280 290 300 310
 AGTEHVLRLDINGVSHLPXLLOAVLGHQPGHVEHLEQGRGATVQOLAPADQXEAHQORPLRERPFQABG
 320 330 340 350 360 370 380
 HHVMSHGLVQAEQRQVVVGARDVRAGDDDLRHPALLIPVVLAEVVLQAHRDOVPPVLDVETVGRGDH
 390 400 410 420 430 440 450
 PDGVDQGPPTQLSISHOOQDLFWTLPGAHLAHNSALGFAGISFFXNRYFSTWIFNCGCAGHPVCOQRVPL
 460 470 480 490 500 510 520 530
 VAPTALGARVVTAIVLTAALVHTDQVLVRLTVPALEGREABADIGLEINLAGAPILAWTXGLVPIIV
 540 550 560 570 580 590 600
 RNPEQLRPLRVLEDLPGLLEGALLLALPLQAGRPQLQERVAPAPVQDVGFLGYEDSVRPLRPHVPC
 610 620 630 640 650 660 670
 PSSXGLSDPACSOALKPKQAEPEGLGDHDEISAK
 680 690 700 710

5. US-10-617-619-7 (1-232)
 US-10-030-203-12

Initial Score = 5 Optimized Score = 37 Significance = -0.41
 Residue Identity = 19% Matches = 54 Mismatches = 146
 Gaps = 71 Conservative Substitutions = 0

RPLIYPTGSGSACGAPPHASRRRSPATCSPRXACCRGRSRRSPAREAWSCSGSPAACHST
 10 20 30 40 50 60 70
 PRCRWDRSLXPGSGXPGSWSAHGMGAGCTPVVLGAALMLWRFSRWGLGCLWRPCTCTPCHSAPGAG
 80 90 100 110 120 130 140
 RXGRXPHGTCCTAPPALSWXYAPRRPRTSXTXPGILRGSRPXPKPGSGRSXGCPWVLGGRGLTVP
 150 160 170 180 190 200 210
 PGVQVLGTVMCEFCCHKIWLRIEMWLAGLGLGVALSAXAFATRCTGRPWCTPQSGPRLRSPGSPXRCPS
 220 230 240 250 260 270 280
 GTTCPGSWHVLHCPRRSPCCHPSSRHRTCTPYLGLSLPPSVTAAGSPGSSAGARXAPXAPGWHRGPAA
 290 300 310 320 330 340 350 360
 GPSRXPMRSARRPASSORTSVRAGRAPHGQXPRAGAGAACRCRGMWCPGRTCWGXXPAPPAGSAHPRRAR
 370 380 390 400 410 420 430
 X
 EPKS-----CDKTHTCPAPPELLGSPSVFLF
 440 450 460 470 480 490 500
 XGRAPAPRSGSSXKFCRNSGPRPPRWXSGSPHTLHSPPTGPMADTPLMGTPCPQPGGLGVCHWHFF
 510 520 530 540 550
 -----PPKPDLMISRT-----EVTGVVVDVSHEDPEVKFNWYDVEVHNAKTKPREEQYNSTVRVSVLT
 560 570 580 590 600
 LEXVFFHMDIQLWVCRTPLRPAESTPRGTDRSAMCF-----CCHCSHAHSR-----RSRSHRS
 610 620 630 640 650 660 670 680 690
 VLH--QDWLNGKEYCKVKS---NKALP--AP-----IEKTSKAKGQPREPQVYTLPPSR---DE
 700 710 720 730 740 750 760 770 780 790 800

AGHCASHSSPRRQGRSRVRTGAGCRSPHSGMDLRHTGPHHCKSRRTASSSR--PXRSPGPPRRSTAPP
 560 570 580 590 600 610 620
 LTKQVSLTCLVKGFYPSDIAVESNGQP-----ENNYKTTTPVLSDSGSFFLYSKLTVDKSRWQGNVF
 150 160 170 180 190 200
 CTPSGFGPAAAPPGTRWRAGAGARRGLPPGLRLCEAPASTACPV-----FL--LLRXPRPLQPGSPE
 630 640 650 660 670 680 690
 210 220 230
 SCVMEHEALHNHYTKSLSPGK
 700 710 X
 QAEGRGAXGPRPXNLCKA

6. US-10-617-619-7 (1-232)
 US-10-030-203-12

Initial Score = 5 Optimized Score = 40 Significance = -0.41
 Residue Identity = 21% Matches = 57 Mismatches = 145
 Gaps = 68 Conservative Substitutions = 0

AAAYHLPQDRBLFCVWLCRASCITEHEKTFPCCHLLSTVSLLRKKPESESSTGGVVLXLFSGCPLLH
 10 20 30 40 50 60 70
 STAMSLGXKPLTRQVRLTWFLVSSSRDGRVYTCXSRGCPALALEMVFMSMGAGRALLETLLHLYSLFSPSOWCR
 80 90 100 110 120 130 140
 TVRTLTRYVLLYCSSRGFLVAXCTSTPSTYQNLNTSGSSWLTSTTHVTGVRIMRVLSLFGGKRKTDPG
 150 160 170 180 190 200 210
 PRSGAGHGHHVXVLSQDLGADPGNGARRRTPGRGSRMSFCSHSMYWTETLVYTPKWPTVAQPWQLTMPV
 220 230 240 250 260 270 280
 RYHVPXWVACGPPPLSPAQESLSPSEPAQNMYSVIFGESPTFRDCCRQSWISRGTLSTWSSRAVAPRSS
 290 300 310 320 330 340 350 360
 WPQLTNEKRTKASVLSNVRSGRQRTTWSVRTGWCRRSSAMSWLVVPGTYVGLMTCATRRRLCSSPSCS
 370 380 390 400 410 420 430
 X
 EPKSCDKTHTCP-----PCPAPELLGGPSVF
 440 450 460 470 480
 LFPKP-----KDTLMIS--RTPEVTCVVVDVSHEDPEVKFNWYDVEVHNAKTKPREEQYN-----
 490 500 510 520 530 540 550 560
 LRSCSPSTAIRFLOFLILSKOWAAETQMV-----LIRVPPHNXAPFTNNRTCHGHSPLIGHT
 570 580 590 600 610 620
 ---TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL--PPSRDELTKNQVSLT
 630 640 650 660 670 680 690
 LPPTIRPMGLLAFLFRIGIFPHGYSTVGVQDTPSASREYPS--MHRQERLVPVMSLQCYCQPPFFFTQLSWS
 700 710 720 730 740 750 760 770 780 790 800
 CL-VKGFYPS-----DIATVWESNGQP-----ENNYKTTTPVL--DSGSEFFLYSKLTVDKSRWQGNVPSVSV
 810 820 830 840 850 860 870 880 890 900
 SLVCSQFRPSKAGRKQIXDWSWSLQEPFPHGLEAHWSPSLXEQNSFVLSASL--KISR--ASSKHCSS
 910 920 930 940 950 960 970 980 990
 MHEALHNHYTKSLSPGK
 220 230 X
 LH-----SLSRFGRSSRNALARRRRTPWASWVYTKLXGPGFHGMSRVSPPEALATPPAARQP
 630 640 650 660 670 680 690
 XSPSRQRSLRAWETWMSLQS
 700 710

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|||||370380390400410420430|||||
ALELMLNVPRLMTQDCLQOSRKVGDSNITEYMFACYSKDSKAGSGPHATHYRGTWYLTGIVSWG
370380390400410420430
QGCATVGHFVYRVSYQVIEWLQKLMRSEPRGVLLRAPFGSAPKSCDKTHTCCPCPAPPELLLGGPSVFLF
370380390400410420430
QGCATVGHFVYRVSYQVIEWLQKLMRSEPRGVLLRAPFGSAPKSCDKTHTCCPCPAPPELLLGGPSVFLF
440450460470480490500
PPKPKDTLM:SRTEPVTVCVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREQYNSYTVRVSVLTVLHQDWLN
PPKPKDTLM:SRTEPVTVCVVDVSHEDPEVKFNMYVDGVEVHNNAKTPREQYNSYTVRVSVLTVLHQDWLN
510520530540550560570
GKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
580590600610620630640
GKEYKCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
590600610620630640
ENNYKTPPVLDSDGPFYLYSKLTVDSRWQGNVFCSCVMHEALHNNHYTKSLSPGK
ENNYKTPPVLDSDGPFYLYSKLTVDSRWQGNVFCSCVMHEALHNNHYTKSLSPGK
650660670680690700710
ENNYKTPPVLDSDGPFYLYSKLTVDSRWQGNVFCSCVMHEALHNNHYTKSLSPGKXAA
650660670680690700710
```

2. US-10-617-619-8 (1-641)
US-10-030-203-12

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Initial Score = 11 Optimized Score = 60 Significance = -0.40
Residue Identity = 17% Matches = 77 Mismatches = 299
Gaps = 72 Conservative Substitutions = 0

10 20 30 40 50 60 70
ANAFLLXLRPGSLXRXCKXQCSFXKARXIFKDAKRTKLFWISYSDGQDCASSPCQNGSKDQLQSYICPC
80 90 100 110 120 130 140
LPAFEGRCNETHKDDQLCVNENGGECYSDHTGTKRSCRCHEGYSLLADGVSCPTPTVEYPCGKIPLEKX
150 160 170 180 190 200 210
NASRPGQIRVIGKVCPCGECPWQVLLVNGAQLCGGTINTIIVWSAAHCFDKIKWENLTVLGEHDLSEH
220 230 240 250 260 270 280
DGDSQSRRAVQIIIPSTVYVPGTTHDIALRLHQPWVLTDHVPLCLPRTFSBRTLA--FVRFSLVSGWQO
RPLIITYPTGRGSSACSCAEP--HASRSMRRSSPAATCSCPXACCGRSRRS----
X 10 20 30 40 50
290 300 310 320 330 340 350
LLDRGA----TALMLVNLVRLMTQDCLQOSRKVGDSNITEYMFACYSKDSKAGSGGPHATHYRG
-PAREAWSKSPAAHCSPTPRCRWD--RSLXPGRSXPGSWSAHPGMGAGCTPVVLGAALMLRWFSR-
60 70 80 90 100 110 120
TWYLTG-----IVSWGQCATVGHFG--VYTRVSYQVIEWLQKLMRSEPRGVLLRAPFGSAPK
130 140 150 160 170 180 190
-WLGLGLCWRRPCTCTPCHSAGSAGRXGRXPHGTCCCTAPPAALSWXVAPP--RPRTSXTXPOGLGRSRRPP
420 430 440 450 460 470 480
SCDKTHTCPCPAPPELLLGGPSVFLFPPKPKDTLM:SRTEPVTVCVVDVSHEDPEVKFNMYVDGVEVHNNAK-
RMXPGGSRSGXGCPWVLGGRGLTVPQGVQLGTVMCEFCFKIWAIRIEMGLAGGLGVALSAXAFAPAR
200 210 220 230 240 250 260
-----KPREQYNSYTVRVSVLTVLHQDWLNKGYCKVSNKALPAPIEKTISKAKGQPREQVY
```

```
CTGRPWCTPOSQPLRSPGSPXRRCPSTGTCFSGWHVGLHCPRRSPCCHP-----SSRHRTCTPYLGS
270 280 290 300 310 320
LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGPFYLYSKLTVDSKSR-----WQ
LPPSVTAAGSPGSS-----AGARXAPXAPGFWRHG--PAAGPSRXP--MRSARRPASSQRTSVRAGRGAHQO
330 340 350 360 370 380 390
QGNVFCSCVMHEALHNNHYTKSLSPGK
400 410 X 420 430 440 450
XG-----PRAGAGGAARCRGWCFGRTCWGXPPAPAGSAHPRARXGRAPAPRPSGSSXFCFRNSGP
RRPRWCXSGSPHTTELHSPPTTGPMADTPLMGTCPPQFGVLGVCHWHEFFLEXVFFHMDIQLWVCRTPLPAE
460 470 480 490 500 510 520
STPRGTDRSAMCPCGCHGSTAHSRRSRSHRSAGHPGASHSSGPRRQGRSRYRTGAGFCRSPHSGMDLHRTGP
530 540 550 560 570 580 590
HHCKKSTAGSSPRPXPSPGPPRRSTAPPCTPSPGSPAAAPPGTTRWAGAGAGRGRLPGGLRLCEAPASTA
600 610 620 630 640 650 660 670
CPVELLLRXPXPRLPQGPSPEAQAEGRGAXGFGREPXNLCKA
680 690 700 710
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3. US-10-617-619-8 (1-641)
US-10-030-203-12

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Initial Score = 8 Optimized Score = 39 Significance = -0.41
Residue Identity = 21% Matches = 53 Mismatches = 149
Gaps = 50 Conservative Substitutions = 0

10 20 30 40 50 60 70
GRLSFTRRQGEALLRVVVVQSLMHGHGAXEDVPLPALVHGELAVEEGAVGVQHGRRGLVVLRLPTALPL
80 90 100 110 120 130 140
HGDVAGIEAFDOAGQADLVLGQLIPGNGQGVHLXFSGLPFGFGDGLDGGWEGFVGLDALVLLAIQPLVQD
150 160 170 180 190 200 210
GEDADHTVRAVLLLPRLCLGXMHLMHVAHVVPVELDLRVFVAHVHHACDLRPGDGHGVLGFWGEEEDXRSP
220 230 240 250 260 270 280
QEFRCWARWACVSFVTRFGLCGSKGWSQEDSWAHLXAHELLOPLDLVLDGDPGVHPKVAHGAALAPADDAQK
290 300 310 320 330 340 350 360
VPRAPVVGGMWASTVPRAGVLAIRVAGTEHVLRDIMGVSHLPXLLQAVLGHQPGHVEHHELOQRGATVQOL
370 380 390 400 410 420 430
APAAOXYEAHEGQRPBRPFGQAEGHHMVSEHDHGLVQAEQRDVVVGGARDVRAGDDDLRHPALLIPVLA
440 450 460 470 480 X 490 500
EVVLAHQRDQVPPVLDVFTVGRGDHPDGVQGPPTQLSSIHQQDQLPWTLPFGAHLAP--HNSALGPAGIS
FXXAR-----XIF-----KDAKRTKLFWISYSDG--DQASSPCQNGSKDQLQOSYICFLPAPFGRNC
30 40 50 60 70 80
FFXNRYFSTWIFNCGCAGHPVCQQRVPLVAPTALGALGARVTVALLTAVALVHTDQLVTLVRLTVPALGREA
510 520 530 540 550 560 570
ETHKDDQL-----ICVNEGCGCQYCSDDHTGTKRSCRCHEGYSLLADGVSCPTPTVEYPCGKIPIL--EKRN
580 590 600 610 620 630 640
EADIGLELVLAGAPILAWTGTLPVITVRNPEQLRPLRVLEDLPGLLEG--ALLLALPLQGARQLQERVG
650 660 670 680 690 700 710
150 160 170 180 190 200 210
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390 400 410 420 430 440
-----QVIEWLOKMRSEPRPGVLLRAPPPGSAEPKSCDKTHTCP---PCPAPELLGGPSVFLFPKPKDT
PPASPIRIRRAQILXONSHMPTVPSTXTPGTGVSLFLPPKIQCHPHDLDPKXHMGGG-GREPRRXGQVQ
470 480 490 500 510 520 530
450 460 470 480 490 500 510
LMISRTPEVTC---VVVDVSHEDPEVKFNWYDGVVEHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKE
LVRRRGAGXGCDKAAGAVOQHVP-----CGQPRHPAPGLAEWQ-----GVQV-QLGQSPSPSRR
540 550 560 570 580 590
520 530 540 550 560
YKCKVSNKA-----LPAPTEKTSKAKGQPREPPQVVTL-----PPSRDELTKQVSLTCLVKGY
ENHLOQRAPRTTGVPAPIPGKADQEPGQDLPQQLLSQRHRRGVGEWAAGEQLQDHASRAGLRLLL
600 610 620 630 640 650 660
570 580 590 600 610 X 630
PSDIWESNGQPPENNYKTTTPVL-DSGSEFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLS
PLOOR-----HRGQVQVAGERLLMLRDXGS---AQPLHAEELPLVSGXMSG
670 680 690 700 710
640
PGK

6. US-10-617-619-8 (1-641)
US-10-030-203-12

Initial Score = 7 Optimized Score = 42 Significance = -0.41
Residue Identity = 19% Matches = 62 Mismatches = 187
Gaps = 70 Conservative Substitutions = 0

SFAEISWSPPRGSSAPFLGFRAAWLAQSLRPQEEKHGTCRSGLTSSXPRKPTASTCTGAGAPTRSW
10 20 30 40 50 60 70
RSCGRAPWRGARRSSAPRRPGRSSRRTRGRSCGFLTVMGTSVPQVHARMGAPARTSSSPISASLSR
80 90 100 110 120 130 140
AGTVRRTRMTSXVKTRTAAVSSTAVTTTRAPAPVAGTRGLCWQTGCPAHPQLNHHVEKYLFXKEMPAMP
150 160 170 180 190 200 210
KAEIWMGARCAPKGVHGRSCCWXNELSCVGPXSTPSCWSPPRTVTSKRTGGTXSRCAWSTTSASTTGMGR
220 230 240 250 260 270 280
AGWRRSSSPARTSRAPPTTTSRCASCTSPWSSLTMCPSACPNGRSLRGRWPSCASHWSAAGASCWTVAPR
290 300 310 320 330 340 350 360
PWSSWCSTCPGXPRTACSSHGRWETPQISRSTCSVPATRMAARTPARGTVEAHMPPTTGARGTXRASSAGA
370 380 390 400 410 420 430
X 10 20 30 40 50
ANAFLLXLRPG--SLXRXCKXQCSFXXA-----RXIFKD-----AXRTKLFWISYSDGDCASSPCON
RAAQFWATL-CCTPGSPSTSGCK-SSCAQSHAQESSCEPHFPQSPNLVTKL---THAHRAOHLNSWGDR
440 450 460 470 480 490
60 70 80 90 100 110 120
GGSCCKDQ-LQSVICFLPAFEGRNCEHDKDQLICVNWENGCEQVCSDTHTKRSRC-----HEGYS-LIA
QSSSSPQNPRTPSKSPGLRSHAWWWTATKTL-----RSSSTGTWTAWRCIXPQSRGRSSITTA
500 510 520 530 540 550
DGV-----SCTPTVEYPCGKIPILEKRNAGKPGQIRIVGGKVCPCGECQWQVLLLVNGAQLCGGTLINTIWW
RTVWSASSPSCTRT-GXWARTSARSPTKQPPSRKPSPK--PKG-----SPENXECTPCPHPGMSXPRT---
560 570 580 590 600 610 620
190 200 210 220 230 240 250

VSAACHCFDKIKNWRNLIAVLGEHDLSEHDG-DEQSRRAVQVVIIPSTVYVPGTTNHDIA--LLRLHQPVVLTDH
RSAXPAWSK-----ASIPATSPWSGRANGSRRTTTRPRLPQWPTPTAPSSSTASSPWTRAGSGRTSS
630 640 650 660 670 680
260 270 280 290 X 300 310 320
VVPLCLPPTFSRTLAFFRFSVSGWQLDRGATALEMLVLNVPRLMTQDCLQOSRKVGDSPNITEYMF
HAPXCMELCTTTTTRRA-----SPCLRVDNDRP
690 700 710 X
330 340 350 360 370 380 390 400
AGYSDGSKDCKGDSGGPHATHYRGTYLTGIVSWGQGCATVGHFYTVRSQYVIEWLQKLMRSEPRPGVLL
410 420 430 440 450 460 470
RAPPPGSAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNMYV
480 490 500 510 520 530 540
DGYEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
550 560 570 580 590 600 610
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRWQGNVF
620 630 640
SCSYMHEALHNHYTQKSLSLSPGK